```
   1 CCCGGGCGAG GACCCCTCCA GGATGCAGGT CCCGAACAGC ACCGGCCCGG
  51 ACAACGCGAC GCTGCAGATG CTGCGGAACC CGGCGATCGC GGTGGCCCTG
 101 CCCGTGGTGT ACTCGCTGGT GGCGGCGGTC AGCATCCCGG GCAACCTCTT
 151 CTCTCTGTGG GTGCTGTGCC GGCGCATGGG GCCCAGATCC CCGTCGGTCA
 201 TCTTCATGAT CAACCTGAGC GTCACGGACC TGATGCTGGC CAGCGTGTTG
 251 CCTTTCCAAA TCTACTACCA TTGCAACCGC CACCACTGGG TATTCGGGGT
 301 GCTGCTTTGC AACGTGGTGA CCGTGGCCTT TTACGCAAAC ATGTATTCCA
 351 GCATCCTCAC CATGACCTGT ATCAGCGTGG AGCGCTTCCT GGGGGTCCTG
 401 TACCCGCTCA GCTCCAAGCG CTGGCGCCGC CGTCGTTACG CGGTGGCCGC
 451 GTGTGCAGGG ACCTGGCTGC TGCTCCTGAC CGCCCTGTCC CCGCTGGCGC
 501 GCACCGATCT CACCTACCCG GTGCACGCCC TGGGCATCAT CACCTGCTTC
 551 GACGTCCTCA AGTGGACGAT GCTCCCCAGC GTGGCCATGT GGGCCGTGTT
 601 CCTCTTCACC ATCTTCATCC TGCTGTTCCT CATCCCGTTC GTGATCACCG
 651 TGGCTTGTTA CACGGCCACC ATCCTCAAGC TGTTGCGCAC GGAGGAGGCG
 701 CACGGCCGGG AGCAGCGGAG GCGCGCGGTG GGCCTGGCCG CGGTGGTCTT
 751 GCTGGCCTTT GTCACCTGCT TCGCCCCCAA CAACTTCGTG CTCCTGGCGC
 801 ACATCGTGAG CCGCCTGTTC TACGGCAAGA GCTACTACCA CGTGTACAAG
 851 CTCACGCTGT GTCTCAGCTG CCTCAACAAC TGTCTGGACC CGTTTGTTTA
 901 TTACTTTGCG TCCCGGGAAT TCCAGCTGCG CCTGCGGGAA TATTTGGGCT
 951 GCCGCCGGGT GCCCAGAGAC ACCCTGGACA CGCGCCGCGA GAGCCTCTTC
1001 TCCGCCAGGA CCACGTCCGT GCGCTCCGAG GCCGGTGCGC ACCCTGAAGG
1051 GATGGAGGGA GCCACCAGGC CCGGCCTCCA GAGGCAGGAG AGTGTGTTCT
1101 GAGTCCCGGG GGCGCAGCTT GGAGAGCCGG GGGCGCAGCT TGGAGATCC
1151 GGGGCGCATG GAGAGGCCAC GGTGCCAGAG GTTCAGGGAG AA
```

FIG. 1

FIG. 2. Predict d polypeptide sequence of HG52.

```
  1 MQVPNSTGPD NATLQMLRNP AIAVALPVVY SLVAAVSIPG NLFSLWVLCR
 51 RMGPRSPSVI FMINLSVTDL MLASVLPFQI YYHCNRHHWV FGVLLCNVVT
101 VAFYANMYSS ILTMTCISVE RFLGVLYPLS SKRWRRRRYA VAACAGTWLL
151 LLTALSPLAR TDLTYPVHAL GIITCFDVLK WTMLPSVAMW AVFLFTIFIL
201 LFLIPFVITV ACYTATILKL LRTEEAHGRE QRRRAVGLAA VVLLAFVTCF
251 APNNFVLLAH IVSRLFYGKS YYHVYKLTLC LSCLNNCLDP FVYYFASREF
301 QLRLREYLGC RRVPRDTLDT RRESLFSART TSVRSEAGAH PEGMEGATRP
351 GLQRQESVF
```

```
10                                      30                                       50
CCGGGCGAGGACCCCTCCAGGATGCAGGTCCCGAACAGCACCGGCCCGGACAACGCGACG
                                        MetGlnValProAsnSerThrGlyProAspAsnAlaThr

70                                      90                                      110
CTGCAGATGCTGCGGAACCCGGCGATCGCGGTGGCCCTGCCCGTGGTGTACTCGCTGGTG
LeuGlnMetLeuArgAsnProAlaIleAlaValAlaLeuProValValTyrSerLeuVal

130                                     150                                     170
GCGGCGGTCAGCATCCCGGGCAACCTCTTCTCTCTGTGGGTGCTGTGCCGGCGCATGGGG
AlaAlaValSerIleProGlyAsnLeuPheSerLeuTrpValLeuCysArgArgMetGly

190                                     210                                     230
CCCAGATCCCCGTCGGTCATCTTCATGATCAACCTGAGCGTCACGGACCTGATGCTGGCC
ProArgSerProSerValIlePheMetIleAsnLeuSerValThrAspLeuMetLeuAla

250                                     270                                     290
AGCGTGTTGCCTTTCCAAATCTACTACCATTGCAACCGCCACCACTGGGTATTCGGGGTG
SerValLeuProPheGlnIleTyrTyrHisCysAsnArgHisHisTrpValPheGlyVal

310                                     330                                     350
CTGCTTTGCAACGTGGTGACCGTGGCCTTTTACGCAAACATGTATTCCAGCATCCTCACC
LeuLeuCysAsnValValThrValAlaPheTyrAlaAsnMetTyrSerSerIleLeuThr

370                                     390                                     410
ATGACCTGTATCAGCGTGGAGCGCTTCCTGGGGGTCCTGTACCCGCTCAGCTCCAAGCGC
MetThrCysIleSerValGluArgPheLeuGlyValLeuTyrProLeuSerSerLysArg

430                                     450                                     470
TGGCGCCGCCGTCGTTACGCGGTGGCCGCGTGTGCAGGGACCTGGCTGCTGCTCCTGACC
TrpArgArgArgArgTyrAlaValAlaAlaCysAlaGlyThrTrpLeuLeuLeuLeuThr

490                                     510                                     530
GCCCTGTCCCCGCTGGCGCGCACCGATCTCACCTACCCGGTGCACGCCCTGGGCATCATC
AlaLeuSerProLeuAlaArgThrAspLeuThrTyrProValHisAlaLeuGlyIleIle

550                                     570                                     590
ACCTGCTTCGACGTCCTCAAGTGGACGATGCTCCCCAGCGTGGCCATGTGGGCCGTGTTC
ThrCysPheAspValLeuLysTrpThrMetLeuProSerValAlaMetTrpAlaValPhe
```

Fig.3A

```
     610                 630                 650
CTCTTCACCATCTTCATCCTGCTGTTCCTCATCCCGTTCGTGATCACCGTGGCTTGTTAC
LeuPheThrIlePheIleLeuLeuPheLeuIleProPheValIleThrValAlaCysTyr

     670                 690                 710
ACGGCCACCATCCTCAAGCTGTTGCGCACGGAGGAGGCGCACGGCCGGGAGCAGCGGAGG
ThrAlaThrIleLeuLysLeuLeuArgThrGluGluAlaHisGlyArgGluGlnArgArg

     730                 750                 770
CGCGCGGTGGGCCTGGCCGCGGTGGTCTTGCTGGCCTTTGTCACCTGCTTCGCCCCCAAC
ArgAlaValGlyLeuAlaAlaValValLeuLeuAlaPheValThrCysPheAlaProAsn

     790                 810                 830
AACTTCGTGCTCCTGGCGCACATCGTGAGCCGCCTGTTCTACGGCAAGAGCTACTACCAC
AsnPheValLeuLeuAlaHisIleValSerArgLeuPheTyrGlyLysSerTyrTyrHis

     850                 870                 890
GTGTACAAGCTCACGCTGTGTCTCAGCTGCCTCAACAACTGTCTGGACCCGTTTGTTTAT
ValTyrLysLeuThrLeuCysLeuSerCysLeuAsnAsnCysLeuAspProPheValTyr

     910                 930                 950
TACTTTGCGTCCCGGGAATTCCAGCTGCGCCTGCGGGAATATTTGGGCTGCCGCCGGGTG
TyrPheAlaSerArgGluPheGlnLeuArgLeuArgGluTyrLeuGlyCysArgArgVal

     970                 990                1010
CCCAGAGACACCCTGGACACGCGCCGCGAGAGCCTCTTCTCCGCCAGGACCACGTCCGTG
ProArgAspThrLeuAspThrArgArgGluSerLeuPheSerAlaArgThrThrSerVal

    1030                1050                1070
CGCTCCGAGGCCGGTGCGCACCCTGAAGGGATGGAGGGAGCCACCAGGCCCGGCCTCCAG
ArgSerGluAlaGlyAlaHisProGluGlyMetGluGlyAlaThrArgProGlyLeuGln

    1090                1110                1130
AGGCAGGAGAGTGTGTTCTGAGTCCCGGGGGCGCAGCTTGGAGAGCCGGGGGCGCAGCTT
ArgGlnGluSerValPhe

    1150                1170                1190
GGAGATCCAGGGGCGCATGGAGAGGCCACGGTGCCAGAGGTTCAGGGAGAA
```

Fig.3B

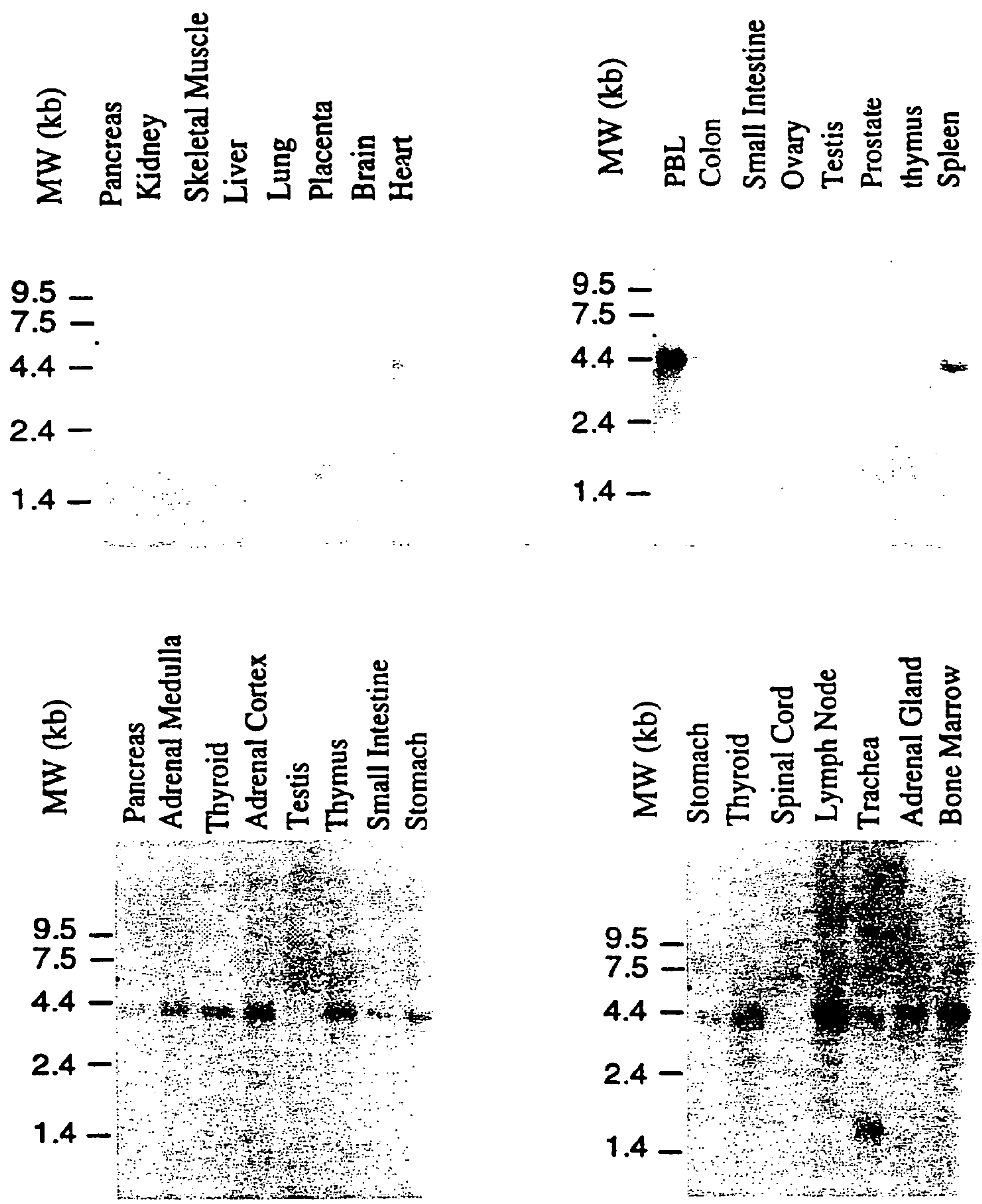
MW (kb)
Pancreas
Kidney
Skeletal Muscle
Liver
Lung
Placenta
Brain
Heart
9.5
7.5
4.4
2.4
1.4
MW (kb)
PBL
Colon
Small Intestine
Ovary
Testis
Prostate
thymus
Spleen
9.5
7.5
4.4
2.4
1.4
MW (kb)
Pancreas
Adrenal Medulla
Thyroid
Adrenal Cortex
Testis
Thymus
Small Intestine
Stomach
9.5
7.5
4.4
2.4
1.4
MW (kb)
Stomach
Thyroid
Spinal Cord
Lymph Node
Trachea
Adrenal Gland
Bone Marrow
9.5
7.5
4.4
2.4
1.4

FIG.4

```
                                        10        20        30
HG52.pep                                MQVPNSTGPDNATLQMLRNPAIAVALPVVYS
                                          |:|   : | :   :| :  ::: :| ||:
hTHRR     EPFWEDEEKNESGLTEYRLVSINKSSPLQKQLPAFISEDASG--YLTSSWLTLFVPSVYT
              60        70        80        90         100       110

            40        50        60        70        80        90
HG52.pep  LVAANVIPGNLFSLWVLCRRMGPRSPSVIFMINLSVTDLMLASVLPFQIYYHCNRHHWVF
           | :||:| |:::: |:  :|  ::|:|::|::|:::|:::::|||||:| |: :    | |
hTHRR     GVFVVSLPLNIMAIVVFILKMKVKKPAVVYMLHLATADVLFVSVLPFKISYYFSGSDWQF
            120       130       140       150       160       170

            100       110       120       130       140       150
HG52.pep  GVLLCNVVTVAFYANMYSSILTMTCISVERFLGVLYPLSSKRWRRRRYAVAACAGTWLLL
          |   ||  ||:||| |||:||| || ||::|||:|:||::|  ||      |  :| : | |
hTHRR     GSELCRFVTAAFYCNMYASILLMTVISIDRFLAVVYPMQSLSWRTLGRASFTCLAIWALA
            180       190       200       210       220       230

           160       170       180       190       200       210
HG52.pep  LTALSPLARTDLTYPVHALGIITCFDVLKWTMLPSVAMWAVFLFTIF-ILLFLIPFVITV
          :::: ||:   : |   | :|:| || |||: |:| :    : :: |: |   ::|::|::|::
hTHRR     IAGVVPLVLKEQTIQVPGLNITTCHDVLNETLLEG---YYAYYFSAFSAVFFFVPLIIST
            240       250       260          270       280

            220       230       240       250       260
HG52.pep  ACYTATILKLLRTEEAHGREQRRRAVGLAAVVLLAFVTCFAPNNFVLLAH--IVSRLFYG
          :||: :|:: | :   : :|  :: ||: |:|:|:   |: ||:|:| :|:||   ::|:
hTHRR     VCYV-SIIRCLSSSAVANRSKKSRALFLSAAVFCIFIICFGPTNVLLIAHYSFLSHTSTT
          290        300       310       320       330       340

         270       280       290       300       310       320
HG52.pep  KSYYHVYKLTLCLSCLNNCLDPFVYYFASREFQLRLREYLGCRRVPRDTLDTRRESLFSA
          :: | :| | :|:| :::|:||::||:|| | |   :    | |::
hTHRR     EAAYFAYLLCVCVSSISSCIDPLIYYYASSECQRYVYSILCCKESSDPSSYNSSGQLMAS
           350       360       370       380       390       400

         330       340       350       360
HG52.pep  RTTSVRSEAGAHPEGMEGATRPGLQRQESVF

hTHRR     KMDTCSSNLNNSIYKKLLT
           410       420
```

FIG.5